



# SEQUENCE LISTING

<110> GOOD, Allen G.  
STROEHER, Virginia L.  
MUENCH, Douglas G.

<120> PLANTS WITH ENHANCED LEVELS OF NITROGEN  
UTILIZATION PROTEINS IN THEIR ROOT EPIDERMIS AND USES  
THEREOF

<130> 595792000420

<140> 10/756,213

<141> 2004-01-12

<150> 10/321,718

<151> 2002-12-17

<150> 09/493,803

<151> 2000-01-28

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 365

<212> DNA

<213> Brassica napus

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aacagctcag ctttcgtttt cggccaatc gctgttccaa ctttacttac aagtcgtaca 180
cgtctctctc tctctctctc tctctcactc acttctctt ataaagactc tctgatcaaa 240
cgtataatcg gaaaactcca ttctttgata ccatcgataa tactaagaga ggtgattgat 300
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tagag 365
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<212> DNA

<213> Barley

<220>

<221> CDS

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Met Ala Ala Thr Val Ala Val
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1

5

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gac aac ctg aac ccc aag gtt tta aaa tgt gag tat gct gtg cgt gga 163
Asp Asn Leu Asn Pro Lys Val Leu Lys Cys Glu Tyr Ala Val Arg Gly
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10	15	20	
gag att gtc atc cat gct cag cgc ttg cag gaa cag cta aag act caa Glu Ile Val Ile His Ala Gln Arg Leu Gln Glu Gln Leu Lys Thr Gln 25 30 35			211
cca ggg tct cta cct ttt gat gag atc ctc tat tgt aac att ggg aac Pro Gly Ser Leu Pro Phe Asp Glu Ile Leu Tyr Cys Asn Ile Gly Asn 40 45 50 55			259
cca caa tct ctt ggt cag caa cca gtt aca ttc ttc agg gag gtt ctt Pro Gln Ser Leu Gly Gln Gln Pro Val Thr Phe Phe Arg Glu Val Leu 60 65 70			307
gcc ctt tgt gat cat cca gac ctg ttg caa aga gag gaa atc aaa aca Ala Leu Cys Asp His Pro Asp Leu Leu Gln Arg Glu Glu Ile Lys Thr 75 80 85			355
ttg ttc agt gct gat tct att tct cga gca aag cag att ctt gcc atg Leu Phe Ser Ala Asp Ser Ile Ser Arg Ala Lys Gln Ile Leu Ala Met 90 95 100			403
ata cct gga aga gca aca gga gca tac agc cat agc cag ggt att aaa Ile Pro Gly Arg Ala Thr Gly Ala Tyr Ser His Ser Gln Gly Ile Lys 105 110 115			451
gga ctt cgt gat gca att gct tct ggg atc gct tca cga gat gga ttc Gly Leu Arg Asp Ala Ile Ala Ser Gly Ile Ala Ser Arg Asp Gly Phe 120 125 130 135			499
cct gct aat gct gat gac att ttt ctc aca gat gga gca agt cct ggg Pro Ala Asn Ala Asp Asp Ile Phe Leu Thr Asp Gly Ala Ser Pro Gly 140 145 150			547
gtg cac ctg atg atg caa tta ctg ata agg aat gag aaa gat ggc att Val His Leu Met Met Gln Leu Leu Ile Arg Asn Glu Lys Asp Gly Ile 155 160 165			595
ctt gtc ccg att cct cag tac ccc ttg tac tcg gct tcc ata gct ctt Leu Val Pro Ile Pro Gln Tyr Pro Leu Tyr Ser Ala Ser Ile Ala Leu 170 175 180			643
cat ggc gga gct ctt gtc cca tac tat ctc aat gaa tcg acg ggc tgg His Gly Gly Ala Leu Val Pro Tyr Tyr Leu Asn Glu Ser Thr Gly Trp 185 190 195			691
ggt ttg gaa acc tct gat gtt aag aag caa ctt gaa gat gct cgg tca Gly Leu Glu Thr Ser Asp Val Lys Lys Gln Leu Glu Asp Ala Arg Ser 200 205 210 215			739
aga ggc atc aac gtt agg gct ttg gtg gtt atc aat cca gga aat cca Arg Gly Ile Asn Val Arg Ala Leu Val Val Ile Asn Pro Gly Asn Pro 220 225 230			787
act gga cag gta ctt gct gaa gaa aac caa tat gac ata gtg aag ttc Thr Gly Gln Val Leu Ala Glu Glu Asn Gln Tyr Asp Ile Val Lys Phe 235 240 245			835

tgc aaa aat gag ggt ctt gtt ctt cta gct gat gag gta tac caa gag	883
Cys Lys Asn Glu Gly Leu Val Leu Leu Ala Asp Glu Val Tyr Gln Glu	
250 255 260	
aac atc tat gtt gac aac aag aaa ttc cac tct ttc aag aag ata gtg	931
Asn Ile Tyr Val Asp Asn Lys Lys Phe His Ser Phe Lys Lys Ile Val	
265 270 275	
aga tcc ttg gga tac ggc gag gag gat ctc cct cta gta tca tat caa	979
Arg Ser Leu Gly Tyr Gly Glu Glu Asp Leu Pro Leu Val Ser Tyr Gln	
280 285 290 295	
tct gtt tct aag gga tat tat ggt gag tgt ggt aaa aga ggt ggt tac	1027
Ser Val Ser Lys Gly Tyr Tyr Gly Glu Cys Gly Lys Arg Gly Gly Tyr	
300 305 310	
ttt gag att act ggc ttc agt gct cca gta aga gag cag atc tac aaa	1075
Phe Glu Ile Thr Gly Phe Ser Ala Pro Val Arg Glu Gln Ile Tyr Lys	
315 320 325	
ata gca tca gtg aac cta tgc tcc aat atc act ggc cag atc ctt gct	1123
Ile Ala Ser Val Asn Leu Cys Ser Asn Ile Thr Gly Gln Ile Leu Ala	
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agt ctt gtc atg aac cca cca aag gct agt gat gaa tca tac gct tca	1171
Ser Leu Val Met Asn Pro Pro Lys Ala Ser Asp Glu Ser Tyr Ala Ser	
345 350 355	
tac aag gca gaa aaa gat gga atc ctc gca tct tta gct cgt cgt gcg	1219
Tyr Lys Ala Glu Lys Asp Gly Ile Leu Ala Ser Leu Ala Arg Arg Ala	
360 365 370 375	
aag gca ttg gag cat gca ttc aat aaa ctt gag gga att act tgc aac	1267
Lys Ala Leu Glu His Ala Phe Asn Lys Leu Glu Gly Ile Thr Cys Asn	
380 385 390	
gag gct gaa gga gca atg tac gtg ttc cct caa atc tgt ctg cca cag	1315
Glu Ala Glu Gly Ala Met Tyr Val Phe Pro Gln Ile Cys Leu Pro Gln	
395 400 405	
aag gca att gag gct gct aaa gct gct aac aaa gca cct gat gca ttc	1363
Lys Ala Ile Glu Ala Ala Lys Ala Ala Asn Lys Ala Pro Asp Ala Phe	
410 415 420	
tat gct ctt cgt ctc ctc gag tcg act gga atc gtc gtt gtc cct gga	1411
Tyr Ala Leu Arg Leu Leu Glu Ser Thr Gly Ile Val Val Val Pro Gly	
425 430 435	
tca gga ttt ggc cag gtt cct ggc aca tgg cac ttc agg tgc acg atc	1459
Ser Gly Phe Gly Gln Val Pro Gly Thr Trp His Phe Arg Cys Thr Ile	
440 445 450 455	
ctt ccg cag gag gat aag atc ccg gca gtc atc tcc cgc ttc acg gtg	1507
Leu Pro Gln Glu Asp Lys Ile Pro Ala Val Ile Ser Arg Phe Thr Val	
460 465 470	

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Phe His Glu Ala Phe Met Ser Glu Tyr Arg Asp  
475 480

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<212> PRT  
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Gln Glu Gln Leu Lys Thr Gln Pro Gly Ser Leu Pro Phe Asp Glu Ile  
35 40 45  
Leu Tyr Cys Asn Ile Gly Asn Pro Gln Ser Leu Gly Gln Gln Pro Val  
50 55 60  
Thr Phe Phe Arg Glu Val Leu Ala Leu Cys Asp His Pro Asp Leu Leu  
65 70 75 80  
Gln Arg Glu Glu Ile Lys Thr Leu Phe Ser Ala Asp Ser Ile Ser Arg  
85 90 95  
Ala Lys Gln Ile Leu Ala Met Ile Pro Gly Arg Ala Thr Gly Ala Tyr  
100 105 110  
Ser His Ser Gln Gly Ile Lys Gly Leu Arg Asp Ala Ile Ala Ser Gly  
115 120 125  
Ile Ala Ser Arg Asp Gly Phe Pro Ala Asn Ala Asp Asp Ile Phe Leu  
130 135 140  
Thr Asp Gly Ala Ser Pro Gly Val His Leu Met Met Gln Leu Leu Ile  
145 150 155 160  
Arg Asn Glu Lys Asp Gly Ile Leu Val Pro Ile Pro Gln Tyr Pro Leu  
165 170 175  
Tyr Ser Ala Ser Ile Ala Leu His Gly Gly Ala Leu Val Pro Tyr Tyr  
180 185 190  
Leu Asn Glu Ser Thr Gly Trp Gly Leu Glu Thr Ser Asp Val Lys Lys  
195 200 205  
Gln Leu Glu Asp Ala Arg Ser Arg Gly Ile Asn Val Arg Ala Leu Val  
210 215 220  
Val Ile Asn Pro Gly Asn Pro Thr Gly Gln Val Leu Ala Glu Glu Asn  
225 230 235 240  
Gln Tyr Asp Ile Val Lys Phe Cys Lys Asn Glu Gly Leu Val Leu Leu  
245 250 255  
Ala Asp Glu Val Tyr Gln Glu Asn Ile Tyr Val Asp Asn Lys Lys Phe  
260 265 270  
His Ser Phe Lys Lys Ile Val Arg Ser Leu Gly Tyr Gly Glu Glu Asp  
275 280 285  
Leu Pro Leu Val Ser Tyr Gln Ser Val Ser Lys Gly Tyr Tyr Gly Glu  
290 295 300  
Cys Gly Lys Arg Gly Gly Tyr Phe Glu Ile Thr Gly Phe Ser Ala Pro  
305 310 315 320  
Val Arg Glu Gln Ile Tyr Lys Ile Ala Ser Val Asn Leu Cys Ser Asn  
325 330 335  
Ile Thr Gly Gln Ile Leu Ala Ser Leu Val Met Asn Pro Pro Lys Ala

